A new diagnostic to assess information for variance parameter estimation in Multi-Environment Trials

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Overview of talk

1. Key motivation
2. New diagnostic
3. Motivating Durum dataset
4. Simulation Studies to Investigate the Performance of the Diagnostic
5. Conclusion

Acknowledgements

- Research presented here is part of my PhD research.

  Lisle, C., Smith, A., Birrell, C., & Cullis, B. R. (2021). Information Based Diagnostic for Genetic Variance Parameter Estimation in Multi-Environment Trials. Frontiers in Plant Science, 12, 2856.

- PhD title: Information based diagnostics for the optimal construction of Multi-environment trial datasets.
- Special thanks to my supervisors Alison Smith, Carole Birrell, and Brian Cullis.

MET dataset analysis

- Selection of superior varieties is a result of the data analysis from a series of plant variety trials at a number of locations and possibly over several years, which are known as Multi-Environment Trials (METs).
- A 1-stage Factor Analytic Linear Mixed Model (FALMM) (Smith et al., 2001) to model Variety by Environment (VE) effects is considered to be the gold standard.
- Substantial literature demonstrates increased genetic gains from the use of FALMM.
- Ancestral information of the varieties grown in the dataset is often available through a 'pedigree file', allowing the partition of the VE effects into additive and non-additive.
- A FALMM that incorporates pedigree information has also been shown to improve selection accuracy (for example Oakey et al., 2007).

Factor Analytic Linear Mixed Model

- A 1-stage analysis so uses individual plot data combined across all trials in the MET
- The LMM comprises fixed and random effects and errors
- The random effects include
  - genetic: VE effects partitioned into additive (associated with pedigree) and non-additive
  - non-genetic: effects associated with trial designs (eg. replicate blocks) and extraneous variation (rows/columns)
- The errors relate to plot to plot variation within trials

Factor Analytic Linear Mixed Model

- The random effects and errors require variance models
  - genetic: FA model for between environment additive genetic variance matrix; FA model for between environment non-additive genetic variance matrix
  - non-genetic: often simple variance components
  - errors: spatial models for each trial (spatial variances, row/column auto-correlations)

- Main focus of MET analysis is accurate prediction of genetic (VE) effects
- Predictions of random effects, including genetic, depend on the variance parameters (genetic, non-genetic and error)
- If we knew the variance parameters we would obtain best linear unbiased predictions (BLUPs) of the genetic effects
- But the variance parameters are unknown so we use residual maximum likelihood (REML, Patterson & Thompson, 1971) estimates obtained from fitting the FALMM

- Use of variance parameter estimates leads to *empirical* best linear unbiased predictions (EBLUPs) of the genetic effects
- EBLUPs are not as accurate as BLUPs
- The (loss in) accuracy for EBLUPs depends on the accuracy/reliability of the REML estimates of the variance parameters (Sales & Hill, 1976)

Key motivation for my research

- Due to the evaluation process, MET datasets are generally (highly) unbalanced.
  $\rightarrow$ most varieties are not present in all environments.
- "Variety Connectivity": the number of varieties in common between environments.
- We observe varying levels of variety connectivity when forming appropriate MET datasets such as the contemporary group methodology of Smith et al. (2021).
  - Dataset is often formed across years and breeding stages.
  - The $\mathcal{A}$-optimality criterion is used to quantify different datasets since this aligns with minimising the probability of an incorrect selection decision (Bueno Filho and Gilmour, 2003).
  - However, this criterion assumes known variance parameters, whereas in practice they are required to be estimated.
- We thought variety connectivity was a key driver of the reliability of genetic variance parameter estimates and that this in turn affected the reliability of predictions of VE effects. **Attributed to the amount of information, or lack there of**.

Variety connectivity

- Variety Connectivity
  - Strong connectivity – many/all varieties in common.
  - Poor connectivity – few (none!) varieties in common.
- Easy to visualise via tables and figures.
- We sometimes exclude environments with poor connectivity from our MET datasets.
- We often suggest ad hoc rules of thumb in regards to the number of varieties that should be present between environments and/or over years.

Investigation of variety connectivity

- Simulation study to investigate the effect of variety connectivity on independent variety effects (Lisle et al., 2018; Lisle et al., 2019).
  - Varied the number of common varieties (m) between trials (1:m).
- Results showed a response in reliability of the Empirical Best Linear Unbiased Predictions (E-BLUPs) over levels of variety connectivity.
  - Correlation between the true (known) and predicted values (those estimated).
- More happening than just the number of varieties in common affecting the performance of variety reliabilities.
  - Difference in the responses for connected and not connected varieties.
  - Increases in reliability values for larger trial sizes.
  - There were some interesting/unexpected results!

Links with fundamental concepts in experimental design theory

- We want to understand about the reliability of genetic variance parameter estimates.
- We require a diagnostic that outperforms the existing variety connectivity approach and can also account for genetic relationships.
- In model-based design we seek designs that minimises/maximises a chosen criteria.
- These include the so-called alphabet series of optimality criteria $(\mathcal{A}, \mathcal{D}, \mathcal{E}, \dots)$.
- $\mathcal{D}$-value optimality minimises the variance of treatment estimates. This is calculated as the determinant of the variance matrix of treatment effects.
- The $\mathcal{D}$-value measure is therefore applicable to our problem where we want to assess the **variance of estimated variance parameters**.

$\mathcal{D}$-value diagnostic of Lisle et al. (2021)

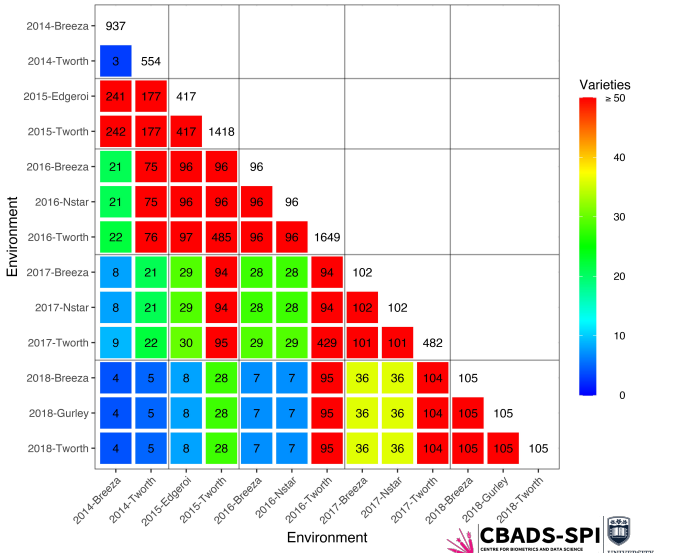
- Calculated as the log-determinant of the partition elements of the inverse expected information matrix for the genetic variance parameters of interest.
  - See Equations (11) and (12) in Lisle et al. (2021).
  - **Warning:** Some heavy algebra!
- We can look at the overall $\mathcal{D}$-value or individual environments ($\mathcal{D}_j$-values).
- Lower diagnostic $\mathcal{D}$-values represent higher levels of information to estimate the parameters of interest. **Lower values are better**.
- Can be investigated over a wide range of models. e.g those with or without genetic relationships information.

Motivating Durum MET dataset

- Selection decisions for Stage 3 (S3) varieties for 2018.
- CG: environments sown between 2014 and 2018 from breeding stages Stage 1 (S1) to S3
- 13 environments, 40 trials, 3,708 varieties, 9,786 plots, 6,168 VE combinations.
  - An environment can comprise of multiple trials which may include different selection stages.
  - We use environment to model VE interaction.
- Number of varieties per environment ranged from 96 to 1,649, with a median of 105.
- Pedigree information was given with 3,959 records.
  - Information for the 3,708 varieties that were grown in the environments and 251 parental varieties that were not grown in the environments.

Variety Connectivity

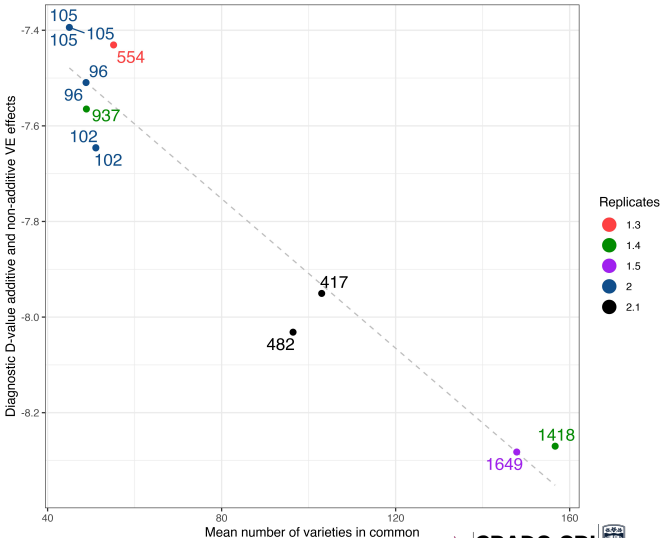
- Can be viewed via figures/tables.
- With ancestral information through the pedigree file, we can also inspect the parental connectivity.
- But there are also common grandparents, cousins, great grandparents etc.
- However, we do not have methods which fully quantify all relationships.



Putting $\mathcal{D}_j$-value into practice: with pedigree information

- We use representative parameter values from historical analyses.
  - 80% additive variance.
  - Between environments correlations of 0.8 for Add/N_Add VE effects.

Environment	$\mathcal{D}_j$-value
2016-Tworth	-8.28
2015-Tworth	-8.27
2017-Tworth	-8.03
2015-Edgeroi	-7.95
2017-Breeza	-7.65
2017-Nstar	-7.65
2014-Breeza	-7.56
2016-Breeza	-7.51
2016-Nstar	-7.51
2014-Tworth	-7.43
2018-Breeza	-7.39
2018-Gurley	-7.39
2018-Tworth	-7.39
n_{κ_g}	182



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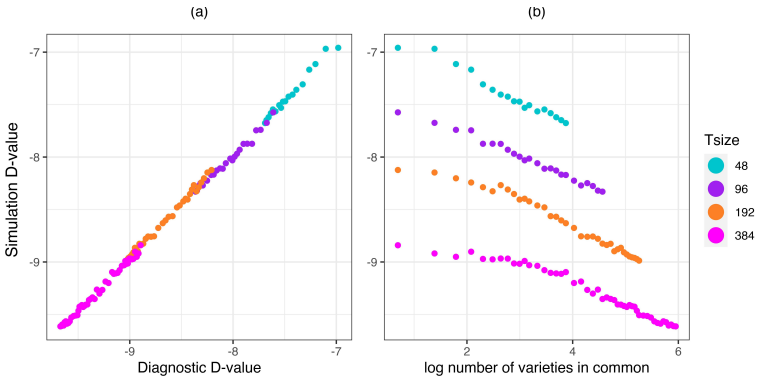
Simulation Studies to Investigate the Performance of the Diagnostic

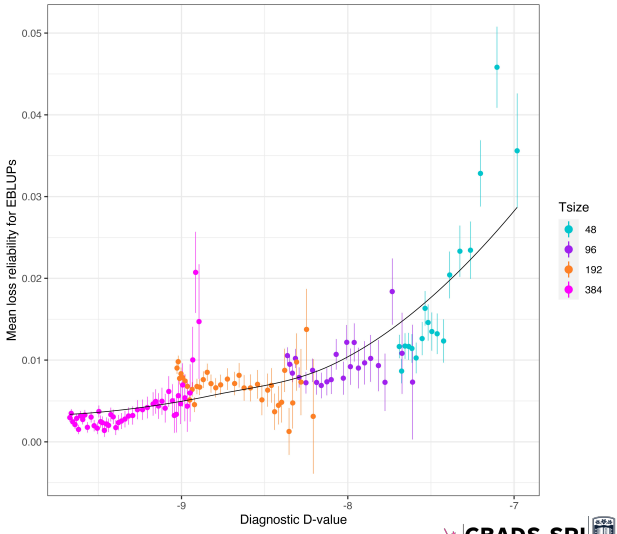
Four trial size (tsize) with $p = 2$ environments, varying the number of varieties in common.

- Genetic relatedness from the durum example.
- $N = 2000$.
- (a) Simulated vs diagnostic $\mathcal{D}$-values show agreement.
- (b) Decreasing linear relationship with (log) variety connectivity, but only within tsize.



Associated loss in EBLUP reliabilities

- Loss is taken as the difference in reliability due to the estimation of variance parameters.
- Smaller trial sizes have a larger associated loss in EBLUP reliabilities.
- The loss is well predicted by the diagnostic $\mathcal{D}$-value.
- This is seen both within and across trial sizes.



Conclusion

- The $\mathcal{D}$-value diagnostic is to be applied to a MET dataset prior to analysis.
- Environments with high $\mathcal{D}$-values may contribute insufficient information for genetic variance parameter estimates, so their inclusion in the MET dataset should be considered.
- Our diagnostic encapsulates not just variety connectivity but also other structural features such as trial size, replication and genetic relatedness.
- Even in the case of 100% connectivity, the smallest trial sizes resulted in large $\mathcal{D}$-values which then translated to substantial losses in the reliability of VE predictions.

Key references

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